

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 25, 2005, 17:08:14 ; search time 499 Seconds

(without alignments)

912.871 Million cell updates/sec

Title: US-10-032-585-7068

Perfect score: 1997

Sequence: 1 MSQQINPDLGSTDIAKLSIP.....QGLDANGNPTGAPAPGAL 390

Scoring table: BIOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 6959266 seqs, 1168006243 residues

Total number of hits satisfying chosen parameters: 6959266

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending Patents AA Main:*

```

1: /cgn2_6/ptodata/7/1/paa/1/ptctis COMB.pep:*
2: /cgn2_6/ptodata/1/paa/1/paa/US06_COMB.pep:*
3: /cgn2_6/ptodata/1/paa/1/paa/US07_COMB.pep:*
4: /cgn2_6/ptodata/1/paa/1/paa/US08_COMB.pep:*
5: /cgn2_6/ptodata/1/paa/1/paa/US01_COMB.pep:*
6: /cgn2_6/ptodata/1/paa/1/paa/US02_COMB.pep:*
7: /cgn2_6/ptodata/1/paa/1/paa/US03_COMB.pep:*
8: /cgn2_6/ptodata/1/paa/1/paa/US04_COMB.pep:*
9: /cgn2_6/ptodata/1/paa/1/paa/US05_COMB.pep:*
10: /cgn2_6/ptodata/1/paa/1/paa/US06_COMB.pep:*
11: /cgn2_6/ptodata/1/paa/1/paa/US087_COMB.pep:*
12: /cgn2_6/ptodata/1/paa/1/paa/US088_COMB.pep:*
13: /cgn2_6/ptodata/1/paa/1/paa/US089_COMB.pep:*
14: /cgn2_6/ptodata/1/paa/1/paa/US090_COMB.pep:*
15: /cgn2_6/ptodata/1/paa/1/paa/US091_COMB.pep:*
16: /cgn2_6/ptodata/1/paa/1/paa/US092_COMB.pep:*
17: /cgn2_6/ptodata/1/paa/1/paa/US093_COMB.pep:*
18: /cgn2_6/ptodata/1/paa/1/paa/US094_COMB.pep:*
19: /cgn2_6/ptodata/1/paa/1/paa/US095_COMB.pep:*
20: /cgn2_6/ptodata/1/paa/1/paa/US096_COMB.pep:*
21: /cgn2_6/ptodata/1/paa/1/paa/US097A_COMB.pep:*
22: /cgn2_6/ptodata/1/paa/1/paa/US097B_COMB.pep:*
23: /cgn2_6/ptodata/1/paa/1/paa/US098_COMB.pep:*
24: /cgn2_6/ptodata/1/paa/1/paa/US099A_COMB.pep:*
25: /cgn2_6/ptodata/1/paa/1/paa/US099B_COMB.pep:*
26: /cgn2_6/ptodata/1/paa/1/paa/US100_COMB.pep:*
27: /cgn2_6/ptodata/1/paa/1/paa/US101_COMB.pep:*
28: /cgn2_6/ptodata/1/paa/1/paa/US102_COMB.pep:*
29: /cgn2_6/ptodata/1/paa/1/paa/US103_COMB.pep:*
30: /cgn2_6/ptodata/1/paa/1/paa/US104_COMB.pep:*
31: /cgn2_6/ptodata/1/paa/1/paa/US105_COMB.pep:*
32: /cgn2_6/ptodata/1/paa/1/paa/US106_COMB.pep:*
33: /cgn2_6/ptodata/1/paa/1/paa/US107_COMB.pep:*
34: /cgn2_6/ptodata/1/paa/1/paa/US108_COMB.pep:*
35: /cgn2_6/ptodata/1/paa/1/paa/US109_COMB.pep:*
36: /cgn2_6/ptodata/1/paa/1/paa/US110_COMB.pep:*
37: /cgn2_6/ptodata/1/paa/1/paa/US60_COMB.pep:*

```

	Result No.	Score	Query Match	Length	DB ID	Description
OM protein - protein search, using sw model	1	1997	100.0	390	1	PCT-US02-03987-15012
Run on: May 25, 2005, 17:08:14 ; search time 499 Seconds (without alignments)	2	1997	100.0	390	26	US-10-032-585-15068
912.871 Million cell updates/sec	3	1997	100.0	390	26	US-10-072-851-15012,
Title: US-10-032-585-7068	4	1997	100.0	390	37	US-60-259-128-1972
Perfect score: 1997	5	1997	100.0	390	37	US-60-314-050-07068
Sequence: 1 MSQQINPDLGSTDIAKLSIP.....QGLDANGNPTGAPAPGAL 390	6	1997	100.0	414	27	US-10-179-131-1485
Scoring table: BIOSUM62	7	1976	98.9	419	32	US-10-603-113-17623
Gapop 10.0 , Gapext 0.5	8	1976	98.9	419	37	Sequence 17623 , A
9: 1214.5	9	60.8	29	387	29	US-10-326-156-117
10: 745	10	37.3	355	1	PCT-US02-131142-3293	
11: 745	11	37.3	355	1	PCT-US04-01099-93380	
12: 745	12	37.3	355	1	Sequence 3380 , AP	
13: 745	13	37.3	355	33	US-10-760-089-33380	
14: 745	14	37.3	355	37	Sequence 3293 , AP	
15: 745	15	37.3	413	20	US-09-675-784A-9454	
16: 695	16	34.8	336	1	PCT-US02-131142-3293	
17: 695	17	34.8	336	27	US-10-128-714-293	
18: 670	18	33.6	338	37	US-60-285-697-2	
19: 670	19	33.6	338	37	US-60-295-890-2	
20: 542	20	27.1	375	1	PCT-US02-40225-3129	
21: 542	21	27.1	375	29	Sequence 3129 , AP	
22: 542	22	27.1	375	37	US-60-341-261-3129	
23: 320.5	23	16.0	344	20	US-09-614-150-3386	
24: 320.5	24	16.0	344	20	Sequence 4386 , AP	
25: 320.5	25	16.0	344	20	Sequence 4469 , AP	
26: 320.5	26	16.0	344	37	Sequence 3662 , AP	
27: 320.5	27	16.0	344	37	Sequence 4464-662	
28: 320.5	28	16.0	344	37	Sequence 3504 , AP	
29: 290	29	14.5	340	20	US-09-614-150-2103	
30: 290	30	14.5	340	20	Sequence 2103 , AP	
31: 290	31	14.5	340	24	Sequence 50 , APPL	
32: 290	32	14.5	340	37	Sequence 2109 , AP	
33: 290	33	14.5	340	37	Sequence 1686 , AP	
34: 263	34	13.2	361	1	PCT-US04-24424-1055	
35: 263	35	13.2	361	27	US-10-170-205B-21742	
36: 263	36	13.2	361	30	US-10-408-765-1604	
37: 263	37	13.2	361	30	Sequence 1604 , AP	
38: 263	38	13.2	361	37	Sequence 1604 , AP	
39: 263	39	13.2	361	37	Sequence 1604 , AP	
40: 263	40	13.2	361	37	Sequence 19817 , AP	
41: 263	41	13.2	361	37	Sequence 11927 , A	
42: 263	42	13.2	361	37	Sequence 11927 , A	
43: 263	43	13.2	361	37	Sequence 11927 , A	
44: 263	44	13.2	361	37	Sequence 1055 , AP	
45: 263	45	13.2	389	1	Sequence 52270 , A	

ALIGNMENTS

RESULT 1 PCT-US02-03987-15012

GENERAL INFORMATION: Sequence 15012, Application PC/TUS0203987 / APPLICANT: Elitra Pharmaceuticals, Inc. / TITLE OF INVENTION: Methods for Identifying the Target of a Compound which Inhibits / TITLE OF INVENTION: Proliferation / FILE REFERENCE: ELITRA-02AVPC / CURRENT APPLICATION NUMBER: PCT/US02/03987 / CURRENT FILING DATE: 2002-02-02 / PRIOR APPLICATION NUMBER: 60/267,636 / PRIOR FILING DATE: 2001-02-09 / NUMBER OF SEQ ID NOS: 15811 / SOFTWARE: FastSeq for Windows Version 4.0 / SEQ ID NO: 15012 / LENGTH: 390 / TYPE: PCT / ORGANISM: Candida albicans / PCT-US02-03987-15012

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

GenCore version 5.1.6
Copyright (C) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 25, 2005, 17:05:48 ; Search time 43 Seconds
(without alignment(s))
677.050 Million cell updates/sec

Title: US-10-032-585-7068

Perfect score: 1997

Sequence: 1 MSQQINPLGSTDIAKLSIP.....QGLVDANGNPIGPAPGAL 390

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:
1: /cgn2_6/ptodata/1/1iaa/5a_COMB.pep:
2: /cgn2_6/ptodata/1/1aa/5b_COMB.pep:
3: /cgn2_6/ptodata/1/1aa/5a_COMB.pep:
4: /cgn2_6/ptodata/1/1aa/6a_COMB.pep:
5: /cgn2_6/ptodata/1/1aa/PCUTUS_COMB.pep:
6: /cgn2_6/ptodata/1/1aa/backfile1_pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	1976	98.9	419	4	US-09-248-796A-17623	Sequence 1763, A
2	329.5	16.5	453	4	US-09-270-767-43715	Sequence 43715, A
3	125.5	6.3	204	4	US-09-270-767-5915	Sequence 59105, A
4	108	5.4	605	4	US-09-48-039A-13002	Sequence 13002, A
5	102	5.1	1037	4	US-09-543-381A-7677	Sequence 7677, A
6	101	5.1	737	4	US-09-771-035-460	Sequence 460, App
7	101	5.1	2032	4	US-09-071-035-458	Sequence 458, App
8	101	5.1	2032	4	US-09-071-035-452	Sequence 462, App
9	101	5.1	2032	4	US-09-071-035-466	Sequence 466, App
10	101	5.1	2054	4	US-09-134-000C-5612	Sequence 6612, App
11	100.5	5.0	609	4	US-09-252-391A-28399	Sequence 28399, A
12	99	5.0	509	4	US-09-583-110-5241	Sequence 5241, App
13	99	5.0	512	4	US-09-107-433-5122	Sequence 5122, App
14	98.5	4.9	1935	4	US-09-53-092-916	Sequence 916, App
15	98.5	4.9	1944	4	US-09-54-016-10929	Sequence 10929, A
16	98	4.9	671	4	US-09-19-452A-468	Sequence 468, App
17	98	4.9	947	4	US-09-438-85A-447	Sequence 447, App
18	97.5	4.9	4563	4	US-09-108-006C-1	Sequence 1, App
19	95.5	4.8	840	4	US-09-079-030-214	Sequence 214, App
20	95.5	4.8	863	4	US-08-16-271-2	Sequence 2, App
21	95.5	4.8	4536	4	US-09-18-422B-27	Sequence 27, App
22	95.5	4.8	4536	4	US-09-079-030-1	Sequence 1, App
23	95.5	4.8	4563	4	US-09-53-092-842	Sequence 842, App
24	95	4.8	477	4	US-09-52-332-7765	Sequence 7765, App
25	95	4.8	653	4	US-09-438-185-730	Sequence 730, App
26	95	4.8	870	2	US-08-26-311-1	Sequence 1, App
27	95	4.8	870	2	US-08-467-527A-1	Sequence 1, App

Result No.	Score	Query	Match	Length	DB ID	Description
1	1976	98.9	419	4	US-09-248-796A-17623	Sequence 1763, A
2	329.5	16.5	453	4	US-09-270-767-43715	Sequence 43715, A
3	125.5	6.3	204	4	US-09-270-767-5915	Sequence 59105, A
4	108	5.4	605	4	US-09-48-039A-13002	Sequence 13002, A
5	102	5.1	1037	4	US-09-543-381A-7677	Sequence 7677, A
6	101	5.1	737	4	US-09-771-035-460	Sequence 460, App
7	101	5.1	2032	4	US-09-071-035-458	Sequence 458, App
8	101	5.1	2032	4	US-09-071-035-452	Sequence 462, App
9	101	5.1	2032	4	US-09-071-035-466	Sequence 466, App
10	101	5.1	2054	4	US-09-134-000C-5612	Sequence 6612, App
11	100.5	5.0	609	4	US-09-252-391A-28399	Sequence 28399, A
12	99	5.0	509	4	US-09-583-110-5241	Sequence 5241, App
13	99	5.0	512	4	US-09-107-433-5122	Sequence 5122, App
14	98.5	4.9	1935	4	US-09-53-092-916	Sequence 916, App
15	98.5	4.9	1944	4	US-09-54-016-10929	Sequence 10929, A
16	98	4.9	671	4	US-09-19-452A-468	Sequence 468, App
17	98	4.9	947	4	US-09-438-85A-447	Sequence 447, App
18	97.5	4.9	4563	4	US-09-108-006C-1	Sequence 1, App
19	95.5	4.8	840	4	US-09-079-030-214	Sequence 214, App
20	95.5	4.8	863	4	US-08-16-271-2	Sequence 2, App
21	95.5	4.8	4536	4	US-09-18-422B-27	Sequence 27, App
22	95.5	4.8	4536	4	US-09-079-030-1	Sequence 1, App
23	95.5	4.8	4563	4	US-09-53-092-842	Sequence 842, App
24	95	4.8	477	4	US-09-52-332-7765	Sequence 7765, App
25	95	4.8	653	4	US-09-438-185-730	Sequence 730, App
26	95	4.8	870	2	US-08-26-311-1	Sequence 1, App
27	95	4.8	870	2	US-08-467-527A-1	Sequence 1, App

ALIGNMENTS

RESULT 1
US-09-248-796A-17623
Sequence 17623, Application US/09248796A
; Patent No. 6747337
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBIC

US/09-248-796A-17623
; Sequence 17623, Application US/09248796A
; Patent No. 6747337
; FILE REFERENCE: 10716-132
; CURRENT FILING DATE: 1999-02-12
; PRIORITY APPLICATION NUMBER: US 60/074,725
; PRIORITY FILING DATE: 1998-02-13
; PRIORITY APPLICATION NUMBER: US 60/096,409
; PRIORITY FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NO: 28308
; SEQ ID NO 17623
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Candida albicans
; US-09-248-796A-17623

Query Match 98.9% ; Score 1976; DB 4; Length 419;
Best Local Similarity 99.5%; Pred. No. 9.8e-197;
Matches 387; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MSQINPPLGSTDAKLSIPTLPIVTTEPKQNLWSSNPVFSYINDVYITINERKRSLG 60
Db 25 MSQINPPLGSTDAKLSIPTLPIVTTEPKQNLWSSNPVFSYINDVYITINERKRSLG 84
Qy 61 LTNPTTENIKEYARDVFLQYFFGLRADLNKAFTSMNPQFTSHTLSIGSNLPAYAF 120
Db 85 LTNPTTENIKEYARDVFLQYFFGLRADLNKAFTSMNPQFTSHTLSIGSNLPAYAF 144
Qy 121 SALATDDFLQGNTDNDLFSGRINYGMDSNSNISKVTLQLAHGPMSMQLQDQYQANDC 180
Db 145 SALATDDFLQGNTDNDLFSGRINYGMDSNSNISKVTLQLAHGPMSMQLQDQYQANDC 204
Qy 181 SINTATLNPNLFSGRINYGMDSNSNISKVTLQLAHGPMSMQLQDQYQANDC 240
Db 205 SINTATLNPNLFSGRINYGMDSNSNISKVTLQLAHGPMSMQLQDQYQANDC 264
Qy 241 AGNTIASQLOQAGLIALSFWRKTDKVAGLETOVATMKQVADLMLGVPFPIVIEGTQ 300
Db 265 AGNTIASQLOQAGLIALSFWRKTDKVAGLETOVATMKQVADLMLGVPFPIVIEGTQ 324

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model
Run on: May 25, 2005, 16:56:27 ; Search time 163 Seconds
(without alignments)
925.378 Million cell updates/sec

Title: US-10-032-585-7068
Perfect score: 1997
Sequence: 1 MSQQINPPLGSTDIAKLISIP.....QGLVDANGNPIFGAPAGAL 390

Scoring table: BLOSUM62
Gapext 0.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04;*

- 1: geneseqtp1980s;*
- 2: geneseqtp1990s;*
- 3: geneseqp2000s;*
- 4: geneseqtp2001s;*
- 5: geneseqtp2002s;*
- 6: geneseqp2003as;*
- 7: geneseqp2003bs;*
- 8: geneseqtp2004s;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	1997	100.0	390	5	ABP73231		Abp73231 Candida a Abr3859 Protein s Adk4914 Disease t
2	1214.5	60.8	387	6	ABR53159		Abj25635 Aspergilll Adr86330 Aspergilll
3	1214.5	60.8	387	7	ADK64914		Abj26235 Aspergilll
4	745	37.3	355	6	ADP25360		Abj70085 C. neofor
5	745	37.3	355	6	ADR86330		Abbr9198 Drosophil
6	695	34.8	336	6	ABJ26235		Abbr8437 Drosophil
7	542	27.1	375	7	ADP70085		Adj37933 D melanog
8	320.5	16.0	344	4	ABB59198		Adj37938 Human hea
9	290	14.5	340	4	ABB58437		Abm2134 Tumour-as
10	290	14.5	340	7	ADJ37933		Abm2134 Tumour-as
11	263	13.2	361	7	ADJ69798		Abm56258 Human PRO
12	263	13.2	361	8	ABMB2134		Adp53360 PRO Polyp
13	263	13.2	361	8	ADP56258		Abp21911 Novel hum
14	263	13.2	361	8	ADP25360		Abp44273 Novel hum
15	263	13.2	389	4	ABG21911		Aag11737 Arabidops
16	258	12.9	314	7	ADJ70870		Aag11738 Arabidops
17	251.5	12.6	349	6	ABR44273		Aag11739 Arabidops
18	242.5	12.1	309	3	AAG11737		Aam33464 Human imm
19	241.5	12.1	309	3	AAG20518		Abp99082 Apolipop
20	241.5	12.1	332	3	AAG20517		Abp95169 Human pro
21	239	12.0	308	4	AAB93239		Abp99244 Human nov
22	239	12.0	308	6	ABG99244		Adi1663 Novel hum
23	239	12.0	318	7	ADI121663		Aag11738 Arabidops
24	234.5	11.7	267	3	AAG11738		Aaw82285 Natural k
25	233.5	11.7	267	3	AAG20919		Aaw8283 Tumour su
			27	217.5	10.9	324	3 AAB58832 Breast an
			28	203	10.2	243	2 AAW8283
			29	199.5	10.0	238	3 AAG11739
			30	188.5	9.4	112	4 AAM83464
			31	175.5	8.8	257	5 ABB99082
			32	171.5	8.6	276	4 ABG21910 Novel hum
			33	160.5	8.0	190	4 AAB95169
			34	123.5	6.2	1333	6 ABU27622
			35	116.5	5.8	322	4 ABB71307 Drosophil
			36	113.5	5.7	1122	6 ABU14859 Protein e
			37	111	5.6	927	6 AAE36312 Moraxella
			38	110.5	5.5	321	4 ABG1971 Novel hum
			39	108	5.4	605	7 ABO65485 Klebsiell
			40	107.5	5.4	276	3 AAG05660
			41	107	5.4	927	4 AAB62110 M. bovis
			42	106.5	5.3	276	3 AAG53428 Arabidops
			43	106.5	5.3	276	5 ABB92164 Herbicida
			44	106	5.3	275	7 ABM74317 DNA clone
			45	105.5	5.3	1935	7 ADD45207 Rat Prote

ALIGNMENTS

RESULT 1
ABP73231

ID ABP73231 standard; protein; 390 AA.
XX
AC ABP73231;

XX DT 30-JAN-2003 (first entry)

XX DB Candida albicans essential protein SEQ ID NO 7068.

XX KW Fungus; yeast; tetracycline; promoter; GRACE strain; biosynthesis;

KW signal transduction; DNA replication; cell division; growth;

KW proliferation; Candida albicans; fungicide; antifungal.

XX OS Candida albicans.

XX PN WO200253728-A2.

XX PD 11-JUL-2002.

XX PP 26-DEC-2001; 2001WO-US49486.

XX PR 29-DEC-2000; 2000US-0259128P.

PR 20-FEB-2001; 2001US-00792024.

PR 22-AUG-2001; 2001US-0314050P.

XX (ELITA) ELITA PHARM INC.

XX PA

XX PI Roemer T, Jiang B, Boone C, Bussey H, Ohlsen KL;

XX XX DR WPI; 2002-566694/60.

DR N-PSDB; ABZ21781.

XX PS Claim 44; SEQ ID NO 7068; 167pp + Sequence Listing; English.

XX CC The invention relates to constructing (M1) a strain of diploid fungal

CC cells in which both alleles of a gene are modified, comprising modifying

CC one allele by insertion or replacement by a cassette having an

CC expressible selectable marker and modifying other allele by

CC recombination, of a promoter replacement fragment with a heterologous

CC promoter, so that expression of the second allele is regulated by the

CC promoter, (M1) is useful for constructing a strain of diploid fungal

CC cells in which both alleles of a gene are modified. The diploid fungal

CC cells having both alleles modified are useful for identifying a gene that